GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

September 13, 2000, 10:17:53; Search time 1505.36 Seconds (without alignments)
1460.611 Million cell updates/sec

C7-0800-18097

Title: William Perfect score:

Sequence:

1 gtcgacccacgcgtccgctc.....aaaaaaaaagggcggccgc 1232

Scoring table:

IDENTITY\_NUC Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters:

1945680

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl: • gb\_om:

9b\_p12:\*
9b\_pr1:\*
9b\_pr2:\*
9b\_pr3:\*
9b\_ro:\*
9b\_sts:\*

gb\_sy:\*
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em\_hum1:\*
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em\_in:\*
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em\_un: em\_v1: gb\_htg1: gb\_htg2: gb\_in1: gb\_in2: em\_ba1: em\_ba2: em\_bu3: em\_hum4: em\_hum4: gb\_htg4: gb\_htg4:

gb\_htg11: gb\_htg11: gb\_htg12: gb\_htg13: gb\_htg14: gb\_htg15: gb\_htg15: gb\_htg16: gb\_htg16: gb\_htg16: gen\_hum6:\*
gb\_htg19:\*
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em\_htg1:\*
em\_htg2:\*
em\_htg3:\*
em\_hum5:\* em\_htq6:\*
em\_htq7:\* gb\_p13:\*
gb\_pr5:\*
gb\_htg8:\*
gb\_htg9:\* em\_htg5:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb\_v12:\*

## SUMMARIES

| 6        | 10       | , ,                | ,                  |                    |                    | 3 C      | o (         | ·        |                    | -4.6               |                    | ,                  | ,                  |        |          | o        |          | O        |          |          | o        | a        |                  | · Committee  | er l                 | NO.                  | Result |
|----------|----------|--------------------|--------------------|--------------------|--------------------|----------|-------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|----------|----------|----------|----------|----------|----------|----------|----------|------------------|--------------|----------------------|----------------------|--------|
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| 240.4    | 248.4    |                    | 30.4               | 240.4              | ) A 60 . O         | 340      | 240         | 248      | 2484               | 240                | 3 4                | ) N                | ) i                | 350    | 250.6    | 250.6    | 250.6    | 250.6    | 251.6    | 252      | 252      | 258.4    | 258.4            | 1201.6       |                      | Score                |        |
| 20.2 2   | 20.21    | 20.2               |                    |                    |                    |          | ٠,          | ) i      | . i                | ) i                | 20.                | ن ر                | ) N                |        | 20.3 1   | 20.3 1   | 20.3 1   | 20.3     | 20.4     | 20.5     | 20.5     | 21.0     | 21.0             | 97.5         | X                    | Score · Match Length | Query  |
| 26916    | 172010   | 126228             | 113843             | 90832              | 20000              | 204/00   | 100100      | 00165    | 10000              | 20000              | 2000               | 676107             |                    | 50000  | 185380   | 179392   | L78035   | 99294    | 155323   | 186867   | 177694   | 158440   | 127766           | 199356       |                      | Length               |        |
| 39       | 67       | 4                  |                    | -                  |                    |          |             | ه د<br>۱ |                    | ) <u> </u>         |                    | 6                  | ţ                  |        | 72       | 75       | 61       | 73       | 8        | 31       | 72       | 56       | 911              | 0            | :                    | DB                   |        |
| AC005066 | AC026541 | AC006543           | AC005033           | AC003065           | AC021094           | ACU20064 | ALLIVIS     | HSUSOMT4 | REPTTON            | AC004590           | HS465N24           | AL1591//           | ACUZZZYO           | 300000 | AC015941 | AC026620 | AC021852 | AC008704 | AC009824 | AP000902 | AC019358 | AC008437 | AC005723         | AL160290     |                      | ID                   |        |
| 5 Homo   | _<br>포   | AC006543 , complet | AC005033 Homo sap1 | AC003065 Homo sapi | AC021094 Homo sapi | Homo     | Homo        | Homo     | AC011498 Homo sap1 | AC004590 Homo sapi | ALO31432 Human DNA | AL159177 Homo sapi | AC022290 Homo sapi | HOMO   | 2000     |          | H C      | _        | Homo     | HOMO     | Homo     | Homo     | AC005723 ROMANDI | 8ap1         | これが、これを見るのできるとのできない。 | Description          |        |

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HÖRÖTBEPFENS ***, in unordered pieces.
                     * NOTE: This is a 'unfinished' sequence. It currently * consists of all contigs. The true order of the pleces is * not known and their order in this sequence record is * arbitrary. Where the contigs adjacent to the vector can * be identified, they are labelled with clone_end' in the * feature table. Some order and orientation information * can tentatively be deduced from paired sequencing reads * which have been identified to span the gap between two * contigs. These are labelled as part of the same the contigs.
                                                                                                                                                                                                                                                                                 Assembly program; XGAP4; version 4.5
Sequencing vector: plasmid; LU8752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 174153 bases at least Q40
Consensus quality: 182105 bases at least Q30
Consensus quality: 188197 bases at least Q20
Insert size: 195356; sum-of-contigs
Insert size: 195366; 7.3% error; agarose-fp
Ouality coverage: 2.91x in Q20 bases; sum-of-contigs Quality
Coverage: 2.91x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Sanger Centre
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AC004084 Homo sapi
AL157911 Human chr
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692 Homo sapi
420 Human DNA
795 Homo sapi
819 Homo sapi
31 Homo sapi
31 Homo sapi
31 Homo sapi
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1 1753 contig of 1753 bp in length; fragment_chain 1
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28261 contig of 4130 bp in length; fragment_chain 2 *
37131 contig of 2960 bp in length; fragment_chain 3 *
37131 contig of 2960 bp in length; fragment_chain 3 *
40096 contig of 2820 bp in length; fragment_chain 3 *
43016 contig of 2820 bp in length; fragment_chain 3 *
51780 contig of 7295 bp in length; fragment_chain 3 *
51780 contig of 7295 bp in length; fragment_chain 3 *
51780 contig of 1745 bp in length; fragment_chain 4 *
58176 contig of 1745 bp in length; fragment_chain 4 *
70018 contig of 10450 bp in length; fragment_chain 5 *
779576 contig of 2455 bp in length; fragment_chain 6 *
81979 contig of 233 bp in length; fragment_chain 6 *
81979 contig of 233 bp in length; fragment_chain 7 *
96338 contig of 1345 bp in length; fragment_chain 7 *
96338 contig of 6533 bp in length; fragment_chain 8 *
104736 contig of 10453 bp in length; fragment_chain 8 *
112043 contig of 1746 bp in length; fragment_chain 9 *
122050 contig of 1765 bp in length; fragment_chain 9 *
122050 contig of 5047 bp in length; fragment_chain 10 *
132013 contig of 2870 bp in length; fragment_chain 10 *
132013 contig of 6339 bp in length
13652 contig of 6339 bp in length
163643 contig of 6378 bp in length; fragment_chain 11
181689 contig of 6378 bp in length; fragment_chain 11
181680 contig of 6378 bp in length; fragment_chain 11
181684 contig of 6378 bp in length; fragment_chain 11
181684 contig of 6384 bp in length; fragment_chain 11
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13314 contig of 6708 bp in length; fr
24031 contig of 10617 bp in length;
/note="assembly_fragment:00693
fragment_chain:2"
6607. .13314
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fragment_chain:1"
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fragment_chain:1
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be updated with the finished sequence
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Best Local Similarity 99.7%;
Matches 1204; Conservative
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